ABSTRACT

A technique is disclosed that is useful for determining the presence of specific hybridization expression within an output pattern generated from a digitized image of a biological sample applied to an arrayed platform. The output pattern includes signals associated with noise, and signals associated with the biological sample, some of which are degraded or obscured by noise. The output pattern is first segmented using tessellation. Signal processing, such as interferometry, or more specifically, resonance interferometry, and even more specifically quantum resonance interferometry or stochastic resonance interferometry, is then used to amplify signals associated with the biological sample within the segmented output pattern having an intensity lower than the intensity of signals associated with noise so that they may be clearly distinguished from background noise. The improved detection technique allows repeatable, rapid, reliable, and inexpensive measurements of arrayed platform output patterns.